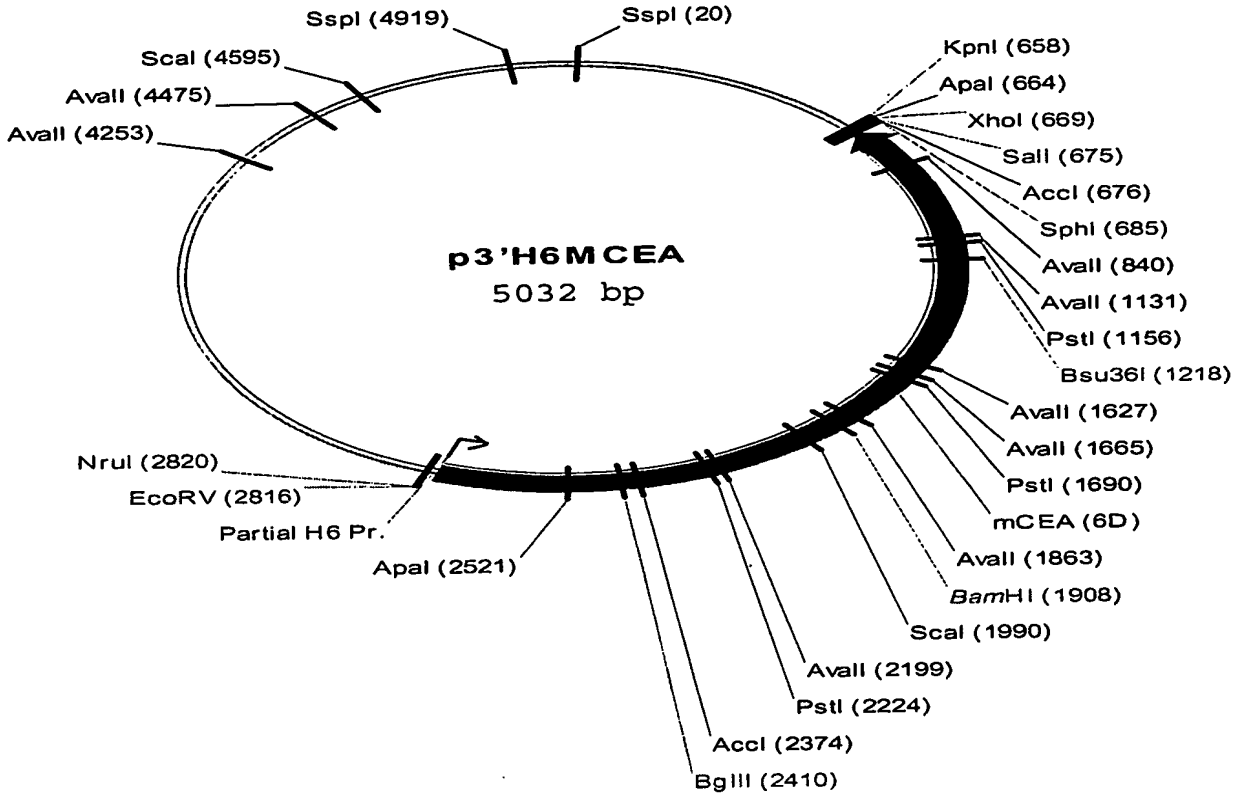
FIGURE 1

A.


SspI (4919)
SspI (20)
ScaI (4595)
AvaII (4475)
AvaII (4253)
KpnI (658)
ApaI (664)
XhoI (669)
SalI (675)
AccI (676)
SphI (685)
AvaII (840)
AvaII (1131)
PstI (1156)
Bsu36I (1218)
AvaII (1627)
AvaII (1665)
PstI (1690)
mCEA (6D)
AvaII (1863)
BamHI (1908)
ScaI (1990)
AvaII (2199)
PstI (2224)
AccI (2374)
BglII (2410)
p3'H6MCEA
5032 bp
NruI (2820)
EcoRV (2816)
Partial H6 Pr.
ApaI (2521)

B.

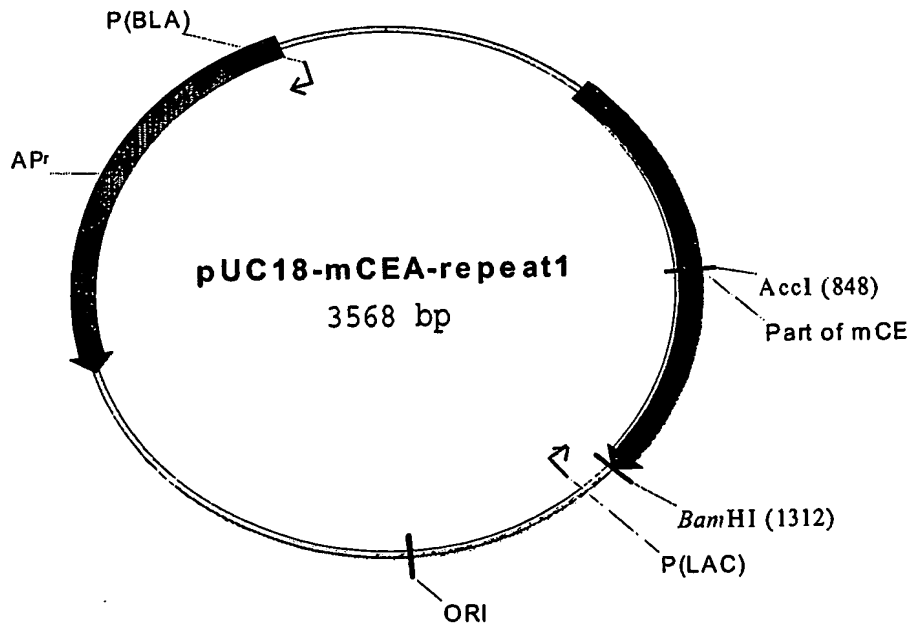
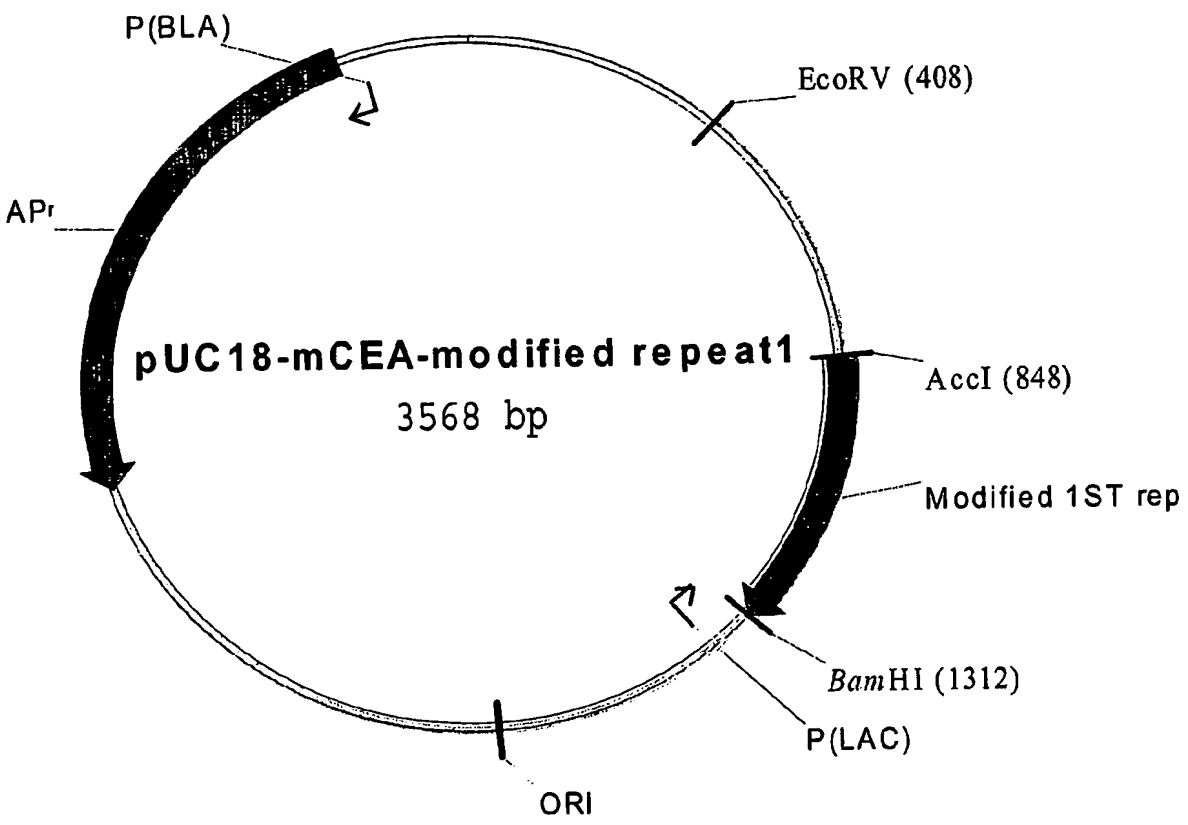
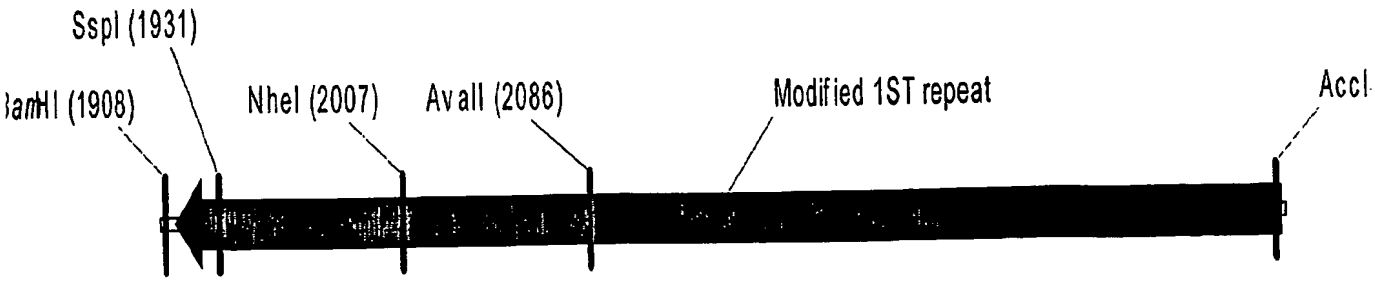

P(BLA)
APr
pUC18-mCEA-repeat1
3568 bp
AccI (848)
Part of mCE
BamHI (1312)
P(LAC)
ORI

FIGURE 2





Fragment of annealed oligos modified repeat 1

471 bp

FIGURE 3

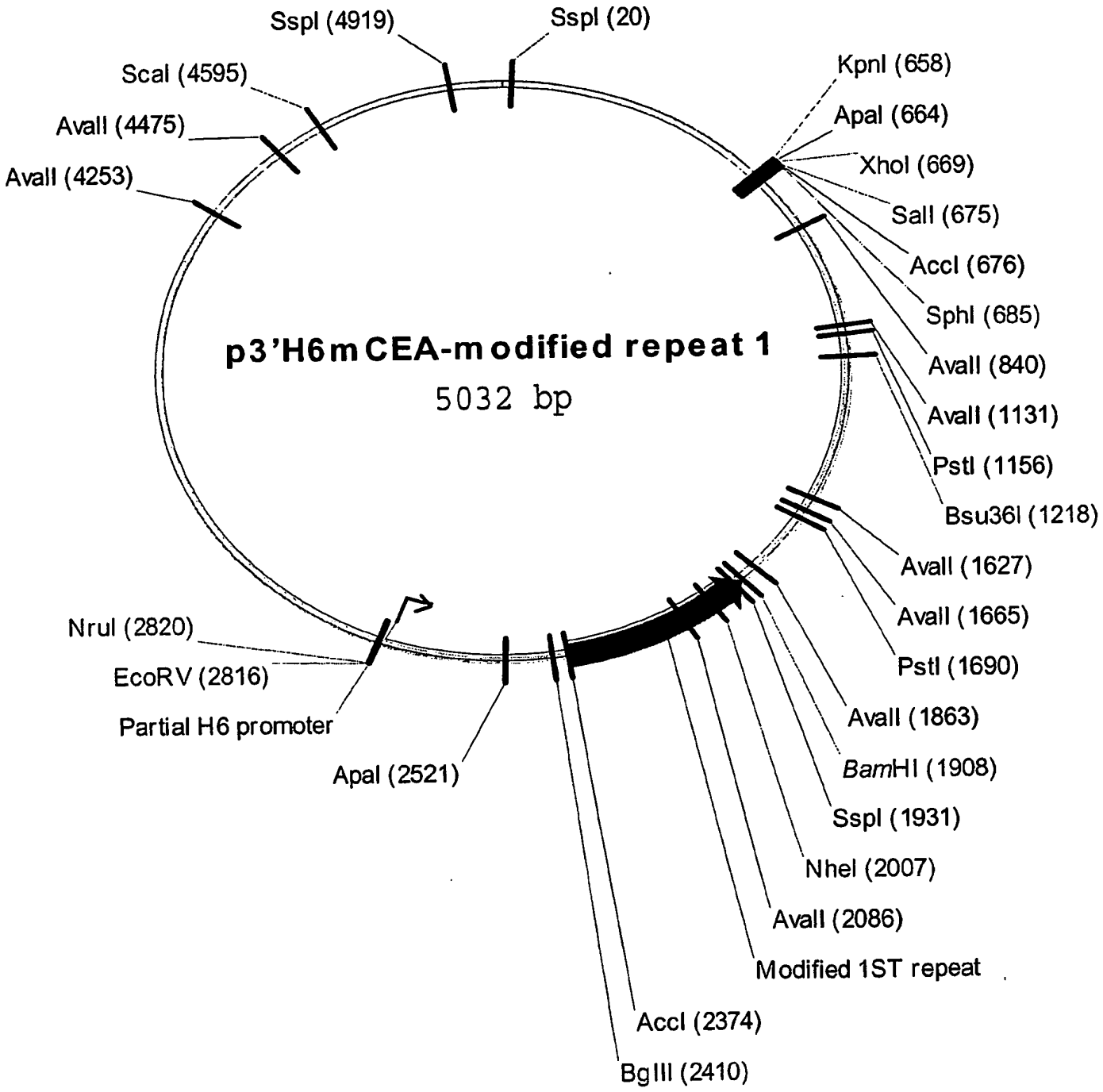

p3'H6mCEA-modified repeat 1
5032 bp
SspI (4919)
SspI (20)
ScaI (4595)
AvaII (4475)
AvaII (4253)
KpnI (658)
ApaI (664)
XhoI (669)
SalI (675)
AccI (676)
SphI (685)
AvaII (840)
AvaII (1131)
PstI (1156)
Bsu36I (1218)
AvaII (1627)
AvaII (1665)
PstI (1690)
AvaII (1863)
BamHI (1908)
SspI (1931)
NheI (2007)
AvaII (2086)
Modified 1ST repeat
AccI (2374)
BglII (2410)
ApaI (2521)
Partial H6 promoter
EcoRV (2816)
NruI (2820)

FIGURE 4

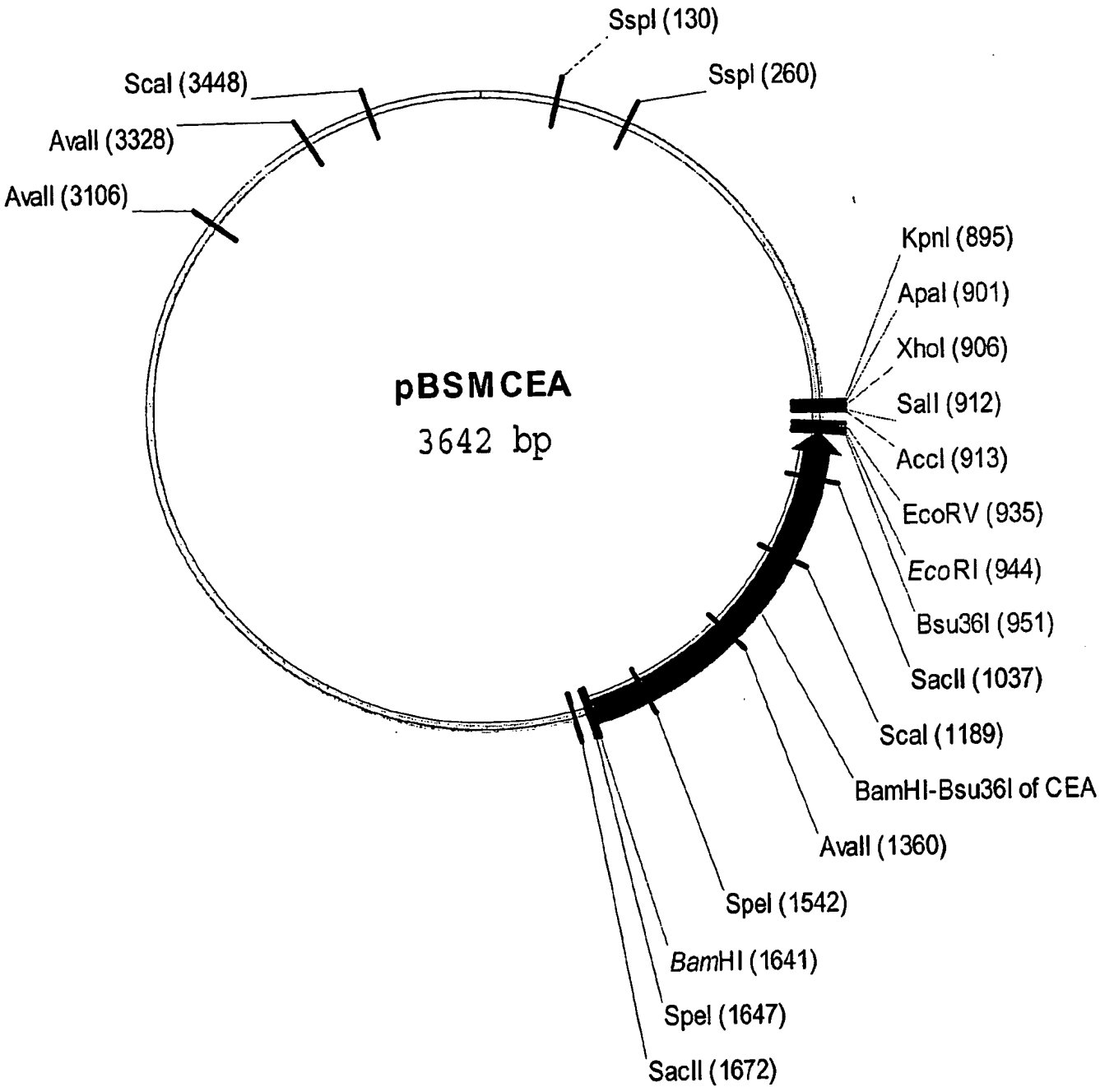
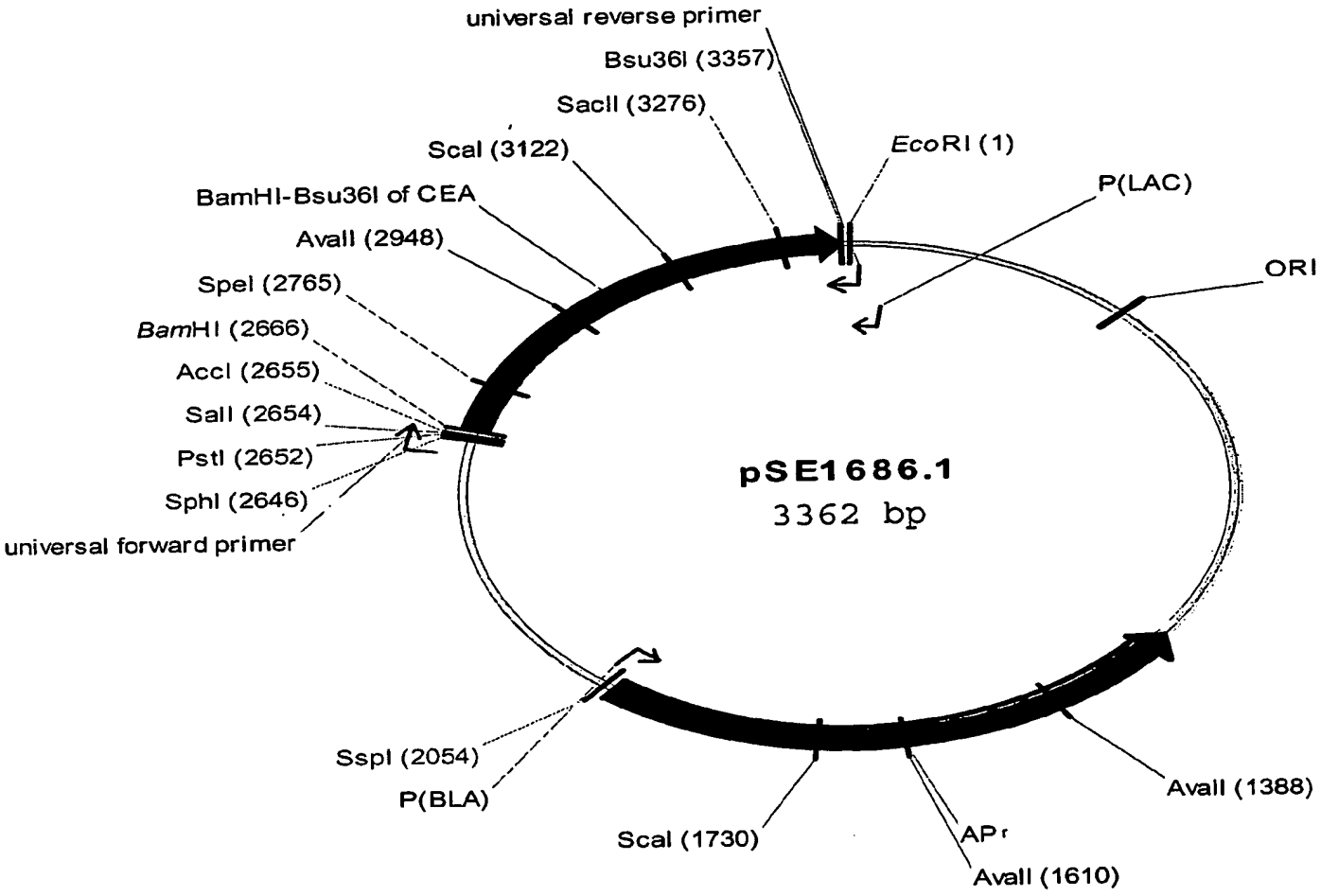
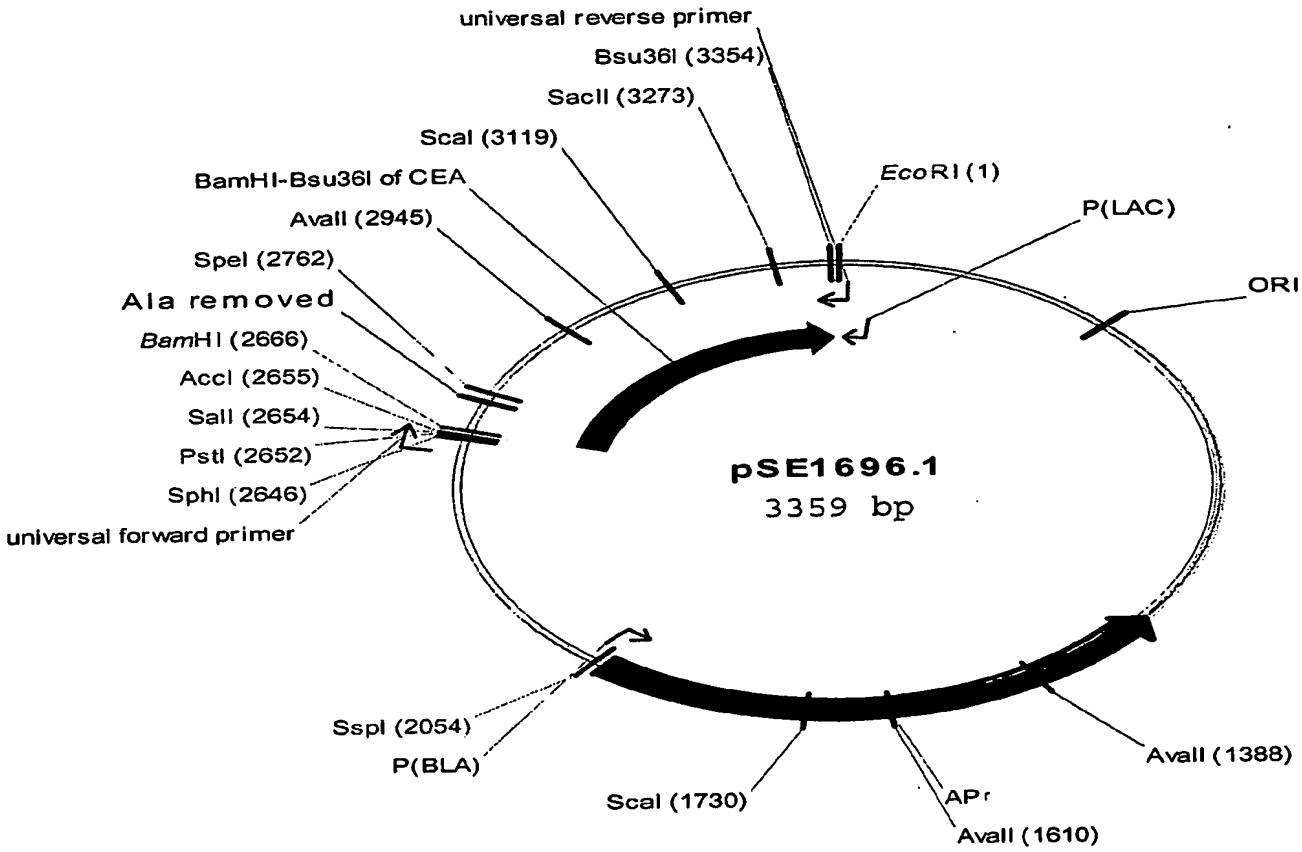

SspI (130)
SspI (260)
ScaI (3448)
AvaII (3328)
AvaII (3106)
pBSMCEA
3642 bp
KpnI (895)
ApaI (901)
XhoI (906)
SalI (912)
AccI (913)
EcoRV (935)
EcoRI (944)
Bsu36I (951)
SacII (1037)
ScaI (1189)
BamHI-Bsu36I of CEA
AvaII (1360)
SpeI (1542)
BamHI (1641)
SpeI (1647)
SacII (1672)

FIGURE 5



pUC18 mCEA modified repeat 2 (gsoe)

FIGURE 6



pUC18 mCEA modified repeat 2 gsoe minus Ala

FIGURE 7

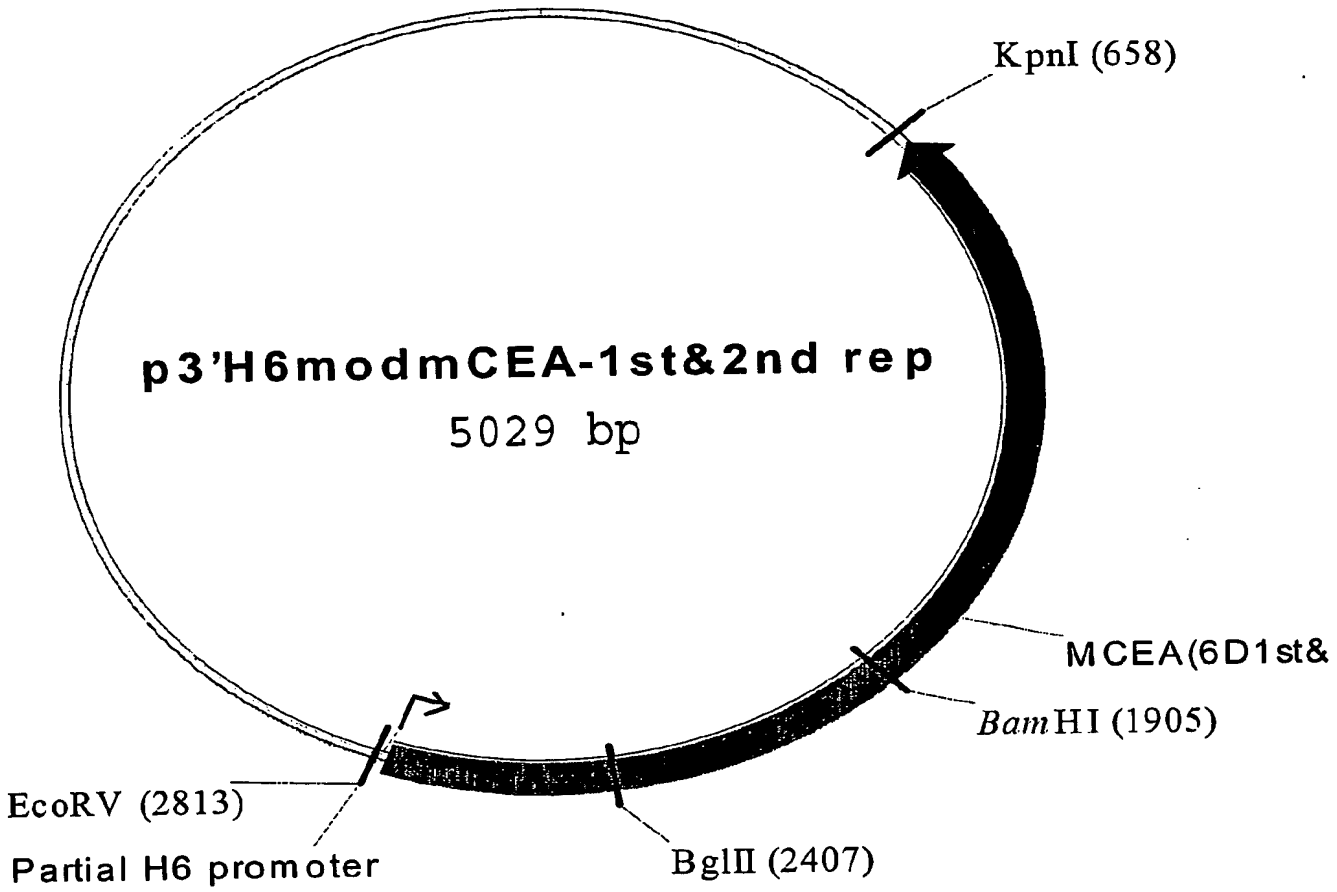

KpnI (658)
p3'H6modmCEA-1st&2nd rep
5029 bp
MCEA(6D1st&
BamHI (1905)
EcoRV (2813)
Partial H6 promoter
BglII (2407)

FIGURE 8

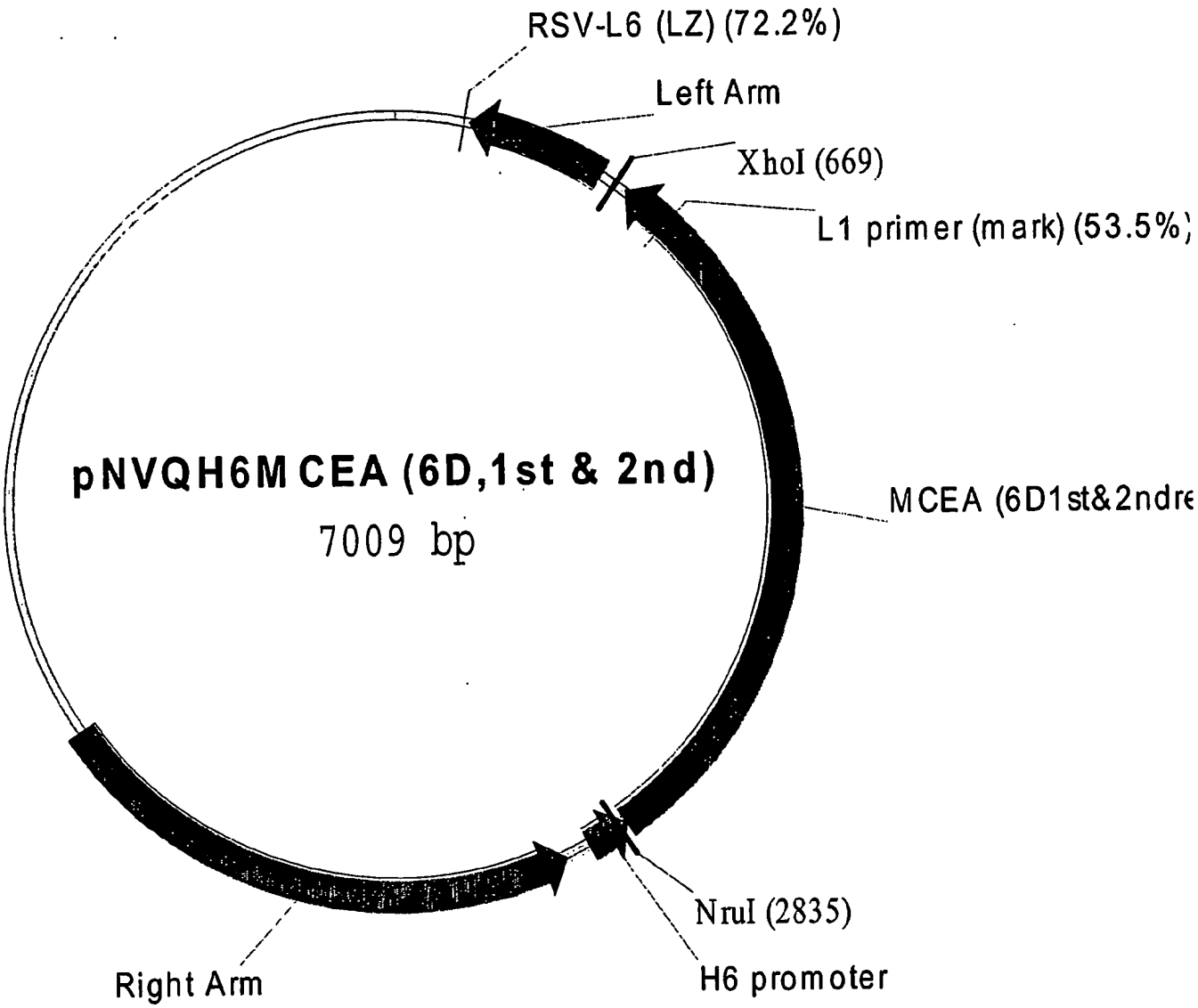

RSV-L6 (LZ) (72.2%)
Left Arm
XhoI (669)
L1 primer (mark) (53.5%)
pNVQH6MCEA (6D,1st & 2nd)
7009 bp
MCEA (6D1st&2ndre
NruI (2835)
H6 promoter
Right Arm

FIGURE 9A

```
                                                                                50
                          1
          mCEA(6D)        ATGGAGTCTC CCTCGGCCCC TCCCCACAGA TGGTGCATCC CCTGGCAGAG
mCEA(6D,1st&2nd)          ATGGAGTCTC CCTCGGCCCC TCCCCACAGA TGGTGCATCC CCTGGCAGAG

                                                                               100
                         51
          mCEA(6D)        GCTCCTGCTC ACAGCCTCAC TTCTAACCTT CTGGAACCCG CCCACCACTG
mCEA(6D,1st&2nd)          GCTCCTGCTC ACAGCCTCAC TTCTAACCTT CTGGAACCCG CCCACCACTG

                                                                               150
                        101
          mCEA(6D)        CCAAGCTCAC TATTGAATCC ACGCCGTTCA ATGTCGCAGA GGGGAAGGAG
mCEA(6D,1st&2nd)          CCAAGCTCAC TATTGAATCC ACGCCGTTCA ATGTCGCAGA GGGGAAGGAG

                                                                               200
                        151
          mCEA(6D)        GTGCTTCTAC TTGTCCACAA TCTGCCCCAG CATCTTTTTG GCTACAGCTG
mCEA(6D,1st&2nd)          GTGCTTCTAC TTGTCCACAA TCTGCCCCAG CATCTTTTTG GCTACAGCTG

                                                                               250
                        201
          mCEA(6D)        GTACAAAGGT GAAAGAGTGG ATGGCAACCG TCAAATTATA GGATATGTAA
mCEA(6D,1st&2nd)          GTACAAAGGT GAAAGAGTGG ATGGCAACCG TCAAATTATA GGATATGTAA

                                                                               300
                        251
          mCEA(6D)        TAGGAACTCA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGATA
mCEA(6D,1st&2nd)          TAGGAACTCA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGATA

                                                                               350
                        301
          mCEA(6D)        ATATACCCCA ATGCATCCCT GCTGATCCAG AACATCATCC AGAATGACAC
mCEA(6D,1st&2nd)          ATATACCCCA ATGCATCCCT GCTGATCCAG AACATCATCC AGAATGACAC

                                                                               400
                        351
          mCEA(6D)        AGGATTCTAC ACCCTACACG TCATAAAGTC AGATCTTGTG AATGAAGAAG
mCEA(6D,1st&2nd)          AGGATTCTAC ACCCTACACG TCATAAAGTC AGATCTTGTG AATGAAGAAG

                                                                               450
                        401
          mCEA(6D)        CAACTGGCCA GTTCCGGGTA TACCCGGAGC TGCCCAAGCC CTCCATCTCC
mCEA(6D,1st&2nd)          CAACTGGCCA GTTCCGGGTA TACCCGGAAC TCCCTAAGCC TTCTATTAGC

                                                                               500
                        451
          mCEA(6D)        AGCAACAACT CCAAACCCGT GGAGGACAAG GATGCTGTGG CCTTCACCTG
mCEA(6D,1st&2nd)          TCCAATAATA GTAAGCCTGT CGAAGACAAA GATGCCGTCG CTTTTACATG

                                                                               550
                        501
          mCEA(6D)        TGAACCTGAG ACTCAGGACG CAACCTACCT GTGGTGGGTA AACAATCAGA
mCEA(6D,1st&2nd)          CGAGCCCGAA ACTCAAGACG CAACATATCT CTGGTGGGTG AACAACCAGT

                                                                               600
                        551
          mCEA(6D)        GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CAGGACCCTC
mCEA(6D,1st&2nd)          CCCTGCCTGT GTCCCCTAGA CTCCAACTCA GCAACGGAAA TAGAACTCTG

                                                                               650
                        601
          mCEA(6D)        ACTCTATTCA ATGTCACAAG AAATGACACA GCAAGCTACA AATGTGAAAC
mCEA(6D,1st&2nd)          ACCCTGTTTA ACGTGACCAG GAACGACACA GCAAGCTACA AATGCGAAAC
```

FIGURE 9B

```
                                651                                                                 700
            mCEA(6D)  CCAGAACCCA GTGAGTGCCA GGCGCAGTGA TTCAGTCATC CTGAATGTCC
mCEA(6D,1st&2nd)  CCAAAATCCA GTCAGCGCCA GGAGGTCTGA TTCAGTGATT CTCAACGTGC

                                701                                                                 750
            mCEA(6D)  TCTATGGCCC GGATGCCCCC ACCATTTCCC CTCTAAACAC ATCTTACAGA
mCEA(6D,1st&2nd)  TTTACGGACC CGATGCTCCT ACAATCAGCC CTCTAAACAC AAGCTATAGA

                                751                                                                 800
            mCEA(6D)  TCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA ACCCACCTGC
mCEA(6D,1st&2nd)  TCAGGGGAAA ATCTGAATCT GAGCTGTCAT GCCGCTAGCA ATCCTCCCGC

                                801                                                                 850
            mCEA(6D)  ACAGTACTCT TGGTTTGTCA ATGGGACTTT CCAGCAATCC ACCCAAGAGC
mCEA(6D,1st&2nd)  CCAATACAGC TGGTTTGTCA ATGGCACTTT CCAACAGTCC ACCCAGGAAC

                                851                                                                 900
            mCEA(6D)  TCTTTATCCC CAACATCACT GTGAATAATA GTGGATCCTA TACGTGCCAA
mCEA(6D,1st&2nd)  TGTTCATTCC CAATATTACC GTGAACAATA GTGGATCCTA CACGTGCCAA

                                901                                                                 950
            mCEA(6D)  GCCCATAACT CAGACACTGG CCTCAATAGG ACCACAGTCA CGACGATCAC
mCEA(6D,1st&2nd)  GCTCACAATA GCGACACCGG ACTCAACCGC ACAACCGTGA CGACGATTAC

                                951                                                                1000
            mCEA(6D)  AGTCTATGAG CCACCCAAAC CCTTCATCAC CAGCAACAAC TCCAACCCCG
mCEA(6D,1st&2nd)  CGTGTATGAG CCACCAAAAC CATTCATAAC TAGTAACAAT TCTAACCCAG

                               1001                                                                1050
            mCEA(6D)  TGGAGGATGA GGATGCTGTA GCCTTAACCT GTGAACCTGA GATTCAGAAC
mCEA(6D,1st&2nd)  TTGAGGATGA GGACGCAGTT GCATTAACTT GTGAGCCAGA GATTCAAAAT

                               1051                                                                1100
            mCEA(6D)  ACAACCTACC TGTGGTGGGT AAATAATCAG AGCCTCCCGG TCAGTCCCAG
mCEA(6D,1st&2nd)  ACCACTTATT TATGGTGGGT CAATAACCAA AGTTTGCCGG TTAGCCCACG

                               1101                                                                1150
            mCEA(6D)  GCTGCAGCTG TCCAATGACA ACAGGACCCT CACTCTACTC AGTGTCACAA
mCEA(6D,1st&2nd)  CTTGCAGTTG TCTAATGATA ACCGCACATT GACACTCCTG TCCGTTACTC

                               1151                                                                1200
            mCEA(6D)  GGAATGATGT AGGACCCTAT GAGTGTGGAA TCCAGAACGA ATTAAGTGTT
mCEA(6D,1st&2nd)  GCAATGATGT AGGACCTTAT GAGTGTGGCA TTCAGAATGA ATTATCCGTT

                               1201                                                                1250
            mCEA(6D)  GACCACAGCG ACCCAGTCAT CCTGAATGTC CTCTATGGCC CAGACGACCC
mCEA(6D,1st&2nd)  GATCACTCCG ACCCTGTTAT CCTTAATGTT TTGTATGGCC CAGACGACCC

                               1251                                                                1300
            mCEA(6D)  CACCATTTCC CCCTCATACA CCTATTACCG TCCAGGGGTG AACCTCAGCC
mCEA(6D,1st&2nd)  AACTATATCT CCATCATACA CCTACTACCG TCCCGGCGTG AACTTGAGCC
```

FIGURE 9C

```
                                                                    1350
                1301
          mCEA(6D) TCTCCTGCCA TGCAGCCTCT AACCCACCTG CACAGTATTC TTGGCTGATT
mCEA(6D,1st&2nd) TTTCTTGCCA TGCAGCATCC AACCCCCCTG CACAGTACTC CTGGCTGATT

                                                                    1400
                1351
          mCEA(6D) GATGGGAACA TCCAGCAACA CACACAAGAG CTCTTTATCT CCAACATCAC
mCEA(6D,1st&2nd) GATGGAAACA TTCAGCAGCA TACTCAAGAG TTATTTATAA GCAACATAAC

                                                                    1450
                1401
          mCEA(6D) TGAGAAGAAC AGCGGACTCT ATACCTGCCA GGCCAATAAC TCAGCCAGTG
mCEA(6D,1st&2nd) TGAGAAGAAC AGCGGACTCT ATACTTGCCA GGCCAATAAC TCAGCCAGTG

                                                                    1500
                1451
          mCEA(6D) GCCACAGCAG GACTACAGTC AAGACAATCA CAGTCTCTGC GGAGCTGCCC
mCEA(6D,1st&2nd) GTCACAGCAG GACTACAGTT AAAACAATAA CTGTTTCCGC GGAGCTGCCC

                                                                    1550
                1501
          mCEA(6D) AAGCCCTCCA TCTCCAGCAA CAACTCCAAA CCCGTGGAGG ACAAGGATGC
mCEA(6D,1st&2nd) AAGCCCTCCA TCTCCAGCAA CAACTCCAAA CCCGTGGAGG ACAAGGATGC

                                                                    1600
                1551
          mCEA(6D) TGTGGCCTTC ACCTGTGAAC CTGAGGCTCA GAACACAACC TACCTGTGGT
mCEA(6D,1st&2nd) TGTGGCCTTC ACCTGTGAAC CTGAGGCTCA GAACACAACC TACCTGTGGT

                                                                    1650
                1601
          mCEA(6D) GGGTAAATGG TCAGAGCCTC CCAGTCAGTC CCAGGCTGCA GCTGTCCAAT
mCEA(6D,1st&2nd) GGGTAAATGG TCAGAGCCTC CCAGTCAGTC CCAGGCTGCA GCTGTCCAAT

                                                                    1700
                1651
          mCEA(6D) GGCAACAGGA CCCTCACTCT ATTCAATGTC ACAAGAAATG ACGCAAGAGC
mCEA(6D,1st&2nd) GGCAACAGGA CCCTCACTCT ATTCAATGTC ACAAGAAATG ACGCAAGAGC

                                                                    1750
                1701
          mCEA(6D) CTATGTATGT GGAATCCAGA ACTCAGTGAG TGCAAACCGC AGTGACCCAG
mCEA(6D,1st&2nd) CTATGTATGT GGAATCCAGA ACTCAGTGAG TGCAAACCGC AGTGACCCAG

                                                                    1800
                1751
          mCEA(6D) TCACCCTGGA TGTCCTCTAT GGGCCGGACA CCCCCATCAT TTCCCCCCCA
mCEA(6D,1st&2nd) TCACCCTGGA TGTCCTCTAT GGGCCGGACA CCCCCATCAT TTCCCCCCCA

                                                                    1850
                1801
          mCEA(6D) GACTCGTCTT ACCTTTCGGG AGCGGACCTC AACCTCTCCT GCCACTCGGC
mCEA(6D,1st&2nd) GACTCGTCTT ACCTTTCGGG AGCGGACCTC AACCTCTCCT GCCACTCGGC

                                                                    1900
                1851
          mCEA(6D) CTCTAACCCA TCCCCGCAGT ATTCTTGGCG TATCAATGGG ATACCGCAGC
mCEA(6D,1st&2nd) CTCTAACCCA TCCCCGCAGT ATTCTTGGCG TATCAATGGG ATACCGCAGC

                                                                    1950
                1901
          mCEA(6D) AACACACACA AGTTCTCTTT ATCGCCAAAA TCACGCCAAA TAATAACGGG
mCEA(6D,1st&2nd) AACACACACA AGTTCTCTTT ATCGCCAAAA TCACGCCAAA TAATAACGGG
```

FIGURE 9D

```
                    1951                                                2000
          mCEA(6D)  ACCTATGCCT GTTTTGTCTC TAACTTGGCT ACTGGCCGCA ATAATTCCAT
mCEA(6D,1st&2nd)    ACCTATGCCT GTTTTGTCTC TAACTTGGCT ACTGGCCGCA ATAATTCCAT

                    2001                                                2050
          mCEA(6D)  AGTCAAGAGC ATCACAGTCT CTGCATCTGG AACTTCTCCT GGTCTCTCAG
mCEA(6D,1st&2nd)    AGTCAAGAGC ATCACAGTCT CTGCATCTGG AACTTCTCCT GGTCTCTCAG

                    2051                                                2100
          mCEA(6D)  CTGGGGCCAC TGTCGGCATC ATGATTGGAG TGCTGGTTGG GGTTGCTCTG
mCEA(6D,1st&2nd)    CTGGGGCCAC TGTCGGCATC ATGATTGGAG TGCTGGTTGG GGTTGCTCTG

                    2101
          mCEA(6D)  ATATAG
mCEA(6D,1st&2nd)    ATATAG
```

FIGURE 10

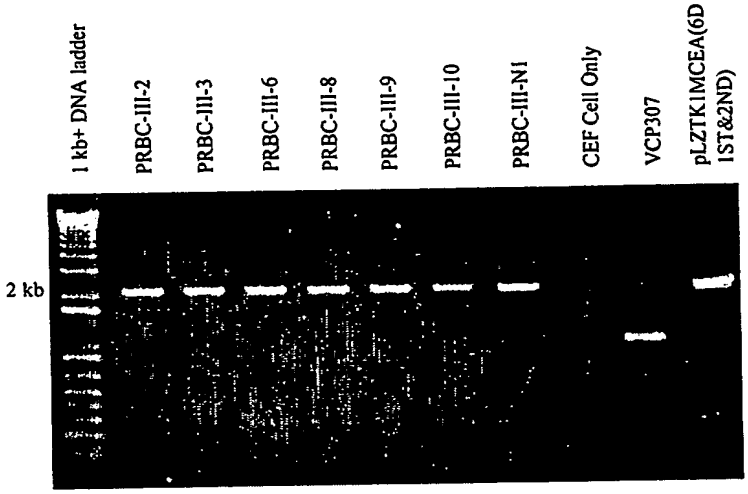
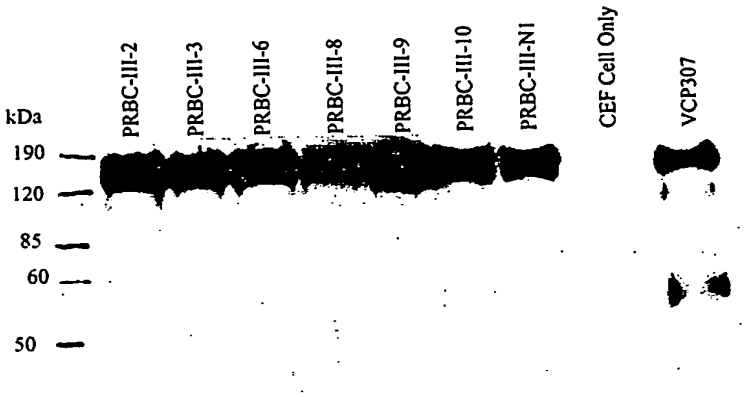

1 kb+ DNA ladder
PRBC-III-2
PRBC-III-3
PRBC-III-6
PRBC-III-8
PRBC-III-9
PRBC-III-10
PRBC-III-N1
CEF Cell Only
VCP307
pLZTK1MCEA(6D 1ST&2ND)
2 kb

FIGURE 11


kDa
190
120
85
60
50
PRBC-III-2
PRBC-III-3
PRBC-III-6
PRBC-III-8
PRBC-III-9
PRBC-III-10
PRBC-III-N1
CEF Cell Only
VCP307